

FIGURE 1

DSP-14

GGCCAGTGGGGGTGGCTGGGCGTGCGGCTGCTACATGCCCCACGGACCAGAACCTCCCGACGCGGCCAGGCCCCGGC  
ACACCCAGCTGCAGAAAGGAGAGAAAATCCCTTGGCTCTAAATGACATCTGGAGAAGTGAAGACAAGCCTCAAGAA  
TGCCTACTCATCTGCCAAGAGGCTGTGCGCGAAGATGGAGGAGGAAGGGGAGGAGGAGGACTACTGCACCCCTGGAG  
CCTTTGAGCTGGAGCGGCTCTTCTGGAAGGGCAGTCCCCAGTACACCCACGTCAACGAGGTCTGGCCCAAGCTCTAC  
ATTGGCGATGAGGCGACGGCGCTGGACCGCTATAGGCTGCAGAAGGCGGGGTTACGCGACGTGCTGAACGCGGCCCA  
CGGCCGCTGGAACGTGGACACTGGGCCCCGACTACTACCGCGACATGGACATCCAGTACCACGGCGTGGAGGCCGACG  
ACCTGCCCACCTTCGACCTCAGTGTCTTCTTCTACCCGGCGGCAGCCTTCATCGACAGAGCGCTAAGCGACGACCAC  
AGTAAGATCCTGGTTCACTGCGTCATGGGCCGAGCCGGTCAGCCACCCCTGGTCCTGGCCTACCTGATGATCCACAA  
GGACATGACCCTGGTGGACGCCATCCAGCAAGTGGCCAAGAACCGCTGCGTCCTCCCGAACCGGGGCTTTTTGAAGC  
AGCTCCGGGAGCTGGACAAGCAGCTGGTGCAGCAGAGGCGACGGTCCCAGCGCCAGGACGGTGAGGAGGAGGATGGC  
AGGGAGCTGTAGGCCCCGACTCACAGGGCCAGCAGAGGCACCTGGGGACAGAGGGGAGAGGCAGAACATAGCCCTGGC  
CTAGGACTCCAGAGAAGGGATGGTGAACCGAAGCTCGACTCTTCCAAACCATCTTGTTCAACTTCCCCATGTGTGC  
TGGGGACAGGGAGGACCCAGAGCTGCCCCGGGCAGAGCTGAGCGCTCAGCCTCTCAGCAAAATGGGAGGGACGGGC  
TCCCCGGCTCTGGGTACAGAGGAGCATGCCACGCTGCACCAAGTCTCCTGCTTTGGTTTTGTTTTTTGGTGAGAA  
GGAAGAGGGAAAAAGATTTTTAAATGTGTAGGCAGTATGTTGTGATTAAACGTTTGGCTTTGTcAAAAAAAAAAAA  
AAAAAAAAAA

FIGURE 1

Translation- 220 amino acids

MTSGEVKTSLKDAYSSAKRLSPKMEEEGEEEDYCTPGAFELERLFWKGSPOYTHVNEVWPPLYIGDEATALDRYRLQ  
KAGFTHVLNAAHGRWNVDTPDYRDMDIQYHGVEADDLPTFDLSVFFYPAAAFIDRALSDDHKILVHCVMGSRRS  
ATLVLAYLMIHKDMTLVDIAIQVAKNRCVLPNRGFLKQLRELDKQLVQQRRRSQRQDGEEDGREL

FIGURE 2

1	10	20	30	40	50	60	70	80	90	100
PYST1	SOLDRD--PNSATDSGSPLSNSQPSFPVEILPFLYLGCAKDSINLDVLEEFGIKYILNVTP-----NLPNLFENAGEFKYKQIPISDHWSQNL									
MKP-7	DRELPSATESDGSPPSSQPAFPVQILPYLYLGCAKDSINLDVLGKYGIKYILNVTP-----NLPNAFEHGGGEFTYKQIPISDHWSQNL									
MKP-4,	GATPPVPYGLRASFPYQILPNHLYLGSARDSANLESIAKLGIKYILNVTP-----NLPNPFKNGDFHYKQIPISDHWSQNL									
hVH5	GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVNLKOLATQNGISYVLNASN-----SCPKNP-DFICESRMRVPINDNYCEKLLPM									
PAC1	PAQALPPAGAENSNSDPRPYTYDQGGPVEILPYLYLGSCHNSSDLQGLQACGITAYLVNSA-----SCPNIHFE--GLFHYKSIIPVEDNQMYEISAM									
MKP-1	PLSTSVPOSAESGSSCSTPLYDQGGPVEILPFLYLGSAYHARSKOMDALGITALLINVSA-----NCPNIHFE--GHYQYKSIIPVEDNHKADISSH									
MKP-2,	PVPPSATEPLDLGSSCGTPLHQGGPVEILPFLYLGSAYHARRDMDALGITALLNVSS-----DCPNHFE--GHYQYKCIIPVEDNHKADISSH									
MKP-5	SERALISQCGKPVNVSYRPAVDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR-----RTSEACH--THLHYKAIIPVEDSHITADISSH									
VHR	SGSFELSVQDLNOLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGI THVLNNAEGRSFMHYNTNANFYKDSGITYLGIKANOTQEFNLSAY									
DSP-14	EGEEEDYCTPGAFELERLFVKGSPQYTHYNEVMPKLYIGDEATALDRYRLQKAGFTHVLNAAHGR---MNVDTIGPDYRYROMDIQYHGVGEADDLPTFDLSVF									
Consensus	.....e!IP.LYIGsa..a.....\$.git.vlNa.....P..f.....%..!p..D.....ls..									
101	110	120	130	140	150	160	170	180	183	
PYST1	FPEATSFIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDITVKMKKSNI									
MKP-7	FPEATSFIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNIS									
MKP-4,	FPEATIEFIDEA-LSQNCGVLVHCLAGVRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNIS									
hVH5	LKDSTIEFIDKA-KLSSCQIVHCLAGISRSATIAIAYTHKTHGSSDDAYRFYKORRPSIS									
PAC1	FQEATSFIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRYLDEAFDFYKORRGV									
MKP-1	FNEATIDFIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRYKLDEAFEFYKQRRSII									
MKP-2,	FMEATIEYIDAV-KOCGRVLVHCQAGISRSATICLAYLMKKRVLEAEFEFYKQRRSII									
MKP-5	FQEATIDFIDCV-REKGGKVLVHCEAGISRSPTICHAAYLMKTKQFLKEAFDYIKQRRSAV									
VHR	FERAADFIDQALAQKNGRVLVHCREGYSRSPITLYIAYLMHRKQHYKSALSTVQRNRE-IGPN									
DSP-14	FYPPAAAFIDRALSDHSHKILVHCYMGRSRSTLVLAYLMITHKONTLVDAIQQVAKNRC-VLPNR									
Consensus	f..ai.FID.a.....!LVHC.aGiSR5.I...aYLM.....n.l.da.....!k..r...!SPNF.F\$gQLI#.#.l.....									

FIGURE 3